RAW SEQUENCE LISTING PATENT APPLICATION US/10/022,366

DATE: 01/17/2002 TIME: 06:57:43

INPUT SET: S36723.raw

This_Raw_Listing-contains-the-General Information Section and up to the first 5 pages. GENERAL INFORMATION: SEQUENCE LISTING 1 2 **Does Not Comply** General Information 3 (1) Corrected Diskette Needed 4 (1) APPLICANT: 7 modup-all responses mu 5 (A) NAME: Boehringer Mannheim GmbH --> 6 7 (B) STREET: Sandhofer Str. 112-132 8 (C) CITY+ Mannheim 9 (E) COUNTRY: Cermany (F) POSTAL CODE: 68305 10 11 (ii) TITLE OF INVENTION: Fanconi-gene II 12 13 CORRESPONDEN
(A) ADDRESSES:
(B) STREET:
(C) CITY:
(D) STATE:
(E) COUNTRY:
(F) ZIP: 14 (iii) NUMBER OF SEQUENCES: 2 15 16 (v) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk 17 (B) COMPUTER: IBM PC compatible 18 (C) OPERATING SYSTEM: PC-DOS/MS-DOS 19 (EPO) 20 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 21 22 (vi) CURRENT APPLICATION DATA (A) APPLICATION NUMBER (US/09/977,801) 23 (B) FILING DATE: 24 25 26 27 (vii) PRIOR APPLICATION DATA: >(A) APPLICATION NUMBER: (A) APPLICATION NUMBER: US/09/402,632 28 (B) FILING DATE: (B) FILING DATE: 29 30 31 (2) INFORMATION FOR SEQ ID NO: 1: 33 34 (i) SEQUENCE CHARACTERISTICS: 35 36 (A) LENGTH: 1026 base pairs (B) TYPE: nucleic acid 37 38 (C) STRANDEDNESS: both (D) TOPOLOGY: linear 39 40 41 (ix) FEATURE: EPO format is invalid for U.S. cases (A) NAME/KEY: CDS 42 43 (B) LOCATION: 256..924 44 45 (ix) FEATURE: (A) NAME/KEY: CDS 46

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47			(B) 1	LOCA	rion:	:430.	.924	<u> </u>					1	INPU'	T SET: S3	36723.raw
48 49	(:	ki-)s:	EQUEI	NCE-I	DESCI	RIPTI	ON:	SEO	ID_N	VO: 1					•	
50																
51 52	TTTCA	CCGTC	TAG	AGGC	ATA A	AGAGG	TGAG	C CC	CGTGC	CTCTI	CAC	GCGGZ	AGAA	GAT	CCCCTAC	60
53 54	CTGGC	CGCCG	GCC	ACTTI	CT C	TGGG	CCGI	G GC	GTC	CTCAA	A GGZ	AGACO	GCC	CTTC	GGCTCA	120
55 56	GGGGC'	rgcgt	TTC	CACAC	CGC G	CCTI	TCCC	'A GO	GCTC	CCGC	GCC	CCGTI	CCT	GCCI	rggccgc	180
57 58	CGGCC	CTCC	AACA	AGCAG	GCA C	AAGG	CGGG	A CI	CAGA	ACCG	GCG	TTC	AGGG	CCGC	CCAGCGG	240
59 60 61 62	CCGCGA	AGGCC	CTG	AG AI Me	G AG et Ar 1	G CI	C CA u Gl	A AG n Ar	A CC g Pr 5	C CG	A CA	AG GC .n Al	a Pr	CG GC CO Al	CG GGT a Gly	291
63 64 65 66 67	GGG AG	G CGC G Arg 15	, Ala	CCC Pro	CGG Arg	GGC Gly	GGG Gly 20	Arg	GGC Gly	TCC Ser	CCC Pro	TAC Tyr 25	Arg	CCA Pro	GAC Asp	339
68 69 70 71	CCG GG Pro Gl	G AGA y Arg 0	GGC Gly	GCG Ala	CGG Arg	AGG Arg 35	Leu	CGA Arg	AGG Arg	TTC Phe	CAG Gln 40	Lys	GGC Gly	GGG Gly	GAG Glu	387
72 73 74 75	GGG GC Gly Al 45	G CCG a Pro	CGC Arg	GCT Ala	GAC Asp 50	Pro	CCC Pro	TGG Trp	GCA Ala	CCG Pro 55	Leu	GGG Gly	ACG Thr	ATG Met	GCG Ala 60	435
76 77 78 79	CTG CT Leu Le	C GCC u Ala	TTG Leu	CTG Leu 65	Leu	GTC Val	GTG Val	GCC Ala	CTA Leu 70	CCG Pro	CGG Arg	GTG Val	TGG Trp	ACA Thr 75	Asp	483
80 81 82 83	GCC AA Ala As	C CYG n Xaa	ACT Thr 80	Ala	AGA Arg	CAA Gln	CGA Arg	GAT Asp 85	CCA Pro	SAG Xaa	GAC Asp	TCC Ser	CAG Gln 90	CGA Arg	ACG Thr	531
84 85 86 87	GAC GA Asp Gl	G GGT u Gly 95	Asp	AAT Asn	AGA Arg	GTG Val	TGG Trp 100	TGT Cys	CAT His	GTT Val	TGT Cys	GAG Glu 105	AGA Arg	GAA Glu	AAC Asn	579
88 89 90 91	ACT TT Thr Ph 11	e Glu O	Cys	Gln	Asn	Pro 115	Arg	Arg	Суѕ	Lys	Trp 120	Thr	Glu	Pro	Tyr	627
92 93 94 95	TGC GT Cys Va 125	l Ile	Ala	Ala	Val 130	Lys	Ile	Phe	Pro	Arg 135	Phe	Phe	Met	Val	Ala 140	675
96 97 98 99	AAG CAG Lys Gl	TGC Cys	TCC Ser	GCT Ala 145	GGT Gly	TGT Cys	GCA Ala	GCG Ala	ATG Met 150	GAG Glu	AGA Arg	CCC Pro	AAG Lys	CCA Pro 155	GAG Glu	723

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														IN	IPUT	SET: S367	23.raw
100	GAG	AAG	CGG	TTT	CTC	CTG	GAA	GAG	CCC	ATG	CCC	TTC	TTT	TAC	CTC	AAG	771
101	Glu	Lys	Arg	Phe	Leu	Leu	Glu	Glu	Pro	Met	Pro	Phe	Phe	Tyr	Leu	Lys	
102				_1.6.0_					1-6-5-					170			
103																	
104	TGT	TGT	AAA	ATT	CGC	TAC	TGC	AAT	TTA	GAG	GGG	CCA	CCT	ATC	AAC	TCA	819
105	Cvs	Cvs	Lvs	Ile	Arq	Tyr	Cys	Asn	Leu	Glu	Gly	Pro	Pro	Ile	Asn	Ser	
106	- 4	-	175		,	-	-	180			-		185				
107																	
108	TCA	GTG	TTC	AAA	GAA	TAT	GCT	GGG	AGC	ATG	GGT	GAG	AGC	TGT	GGT	GGG	867
109						Tyr											
110	501	190		-,0	0_0	- 7 -	195	0-7			0-1	200		-1-	1	<i>1</i>	
111		1) 0.					100										
112	CTC	тсс	СТС	CCC	አጥሮ	CTC	СТС	רידים	CTG	GCC	TCC	Δ ጥጥ	CCA	GCC	ccc	CTC	915
113						Leu											343
	205	тър	пец	мта	116	210	пеа	пец	цец	ALG	215	110	лта	AIG	Gry	220	
114	205					210					2.13					220	
115	700	OTT C	mam	man	7007	aaa /	~ » ~ m/	7007	73 C	, ста	, ~ ~ ~ ~	n m//	7007	~~~ m			964
116				IGA	JCCA	CGG (JACI	3CCA(JA G	4C 1 G2	4GCC.	LIC	MUUU	3CA1			J04
117	ser	ьeu	Ser														
118																	
119	~~~	~~~	~~~	~~ ~~ .	~~~	TG T	~ ~ ~ ~ ~		~ ~~			a mar		~mm /	~~~		7.004
120	GGA	CTCG	CTC (CAGA	CCGT".	rg re	JACC'	rGrrr	¿ CA'.	II.YYY	ACTT.	GT"I".	TTCT	3TT (JAAA	AAAAA	1024
121																	-005
122	AA																1026
123																	
124																	
125	(2)	INF	CAMAC	LION	FOR	SEQ	ID I	10: 2	2:								
126																	
127						CHAI											
128						H: 22			acio	ds							
129	(B) TYPE: amino acids																
130			(1) T(OPOL	OGY:	line	ear									
131																	
132			(ii)	MOLI	ECULI	E TYI	PE: p	prote	ein								
133																	
134			(xi)	SEQ	JENC!	E DES	SCRII	PTIO	1: SI	EQ II	ON C	2:					
135																	
136																	
137	Met	Arg	Leu	Gln	Arg	Pro	Arg	Gln	Ala	Pro	Ala	Gly	Gly	Arg	Arg	Ala	
138	1				5					10					15		
139																	
140	Pro	Arg	Gly	Gly	Arg	Gly	Ser	Pro	Tyr	Arg	Pro	Asp	Pro	Gly	Arg	Gly	
141		_	-	20	_	-			25	_		_		30	_		
142																	
143	Ala	Arg	Arg	Leu	Arg	Arg	Phe	Gln	Lys	Gly	Gly	Glu	Gly	Ala	Pro	Arg	
144			35		,			40	-	•	-		45			-	
145																	
146	Ala	asA	Pro	Pro	Trp	Ala	Pro	Leu	Glv	Thr	Met	Ala	Leu	Leu	Ala	Leu	
147		50			15		55		2			60					
148																	
149	Leu	Leu	Val	Va 1	Ala	Leu	Pro	Ara	Val	Tro	Thr	Asp	Ala	Asn	Xaa	Thr	
150	65					70		9			75					80	
151											. •						
	- 1	_	~ 1			- -	•• • •	-	a	a1			3	~ 1	~1	*	

152 Ala Arg Gln Arg Asp Pro Xaa Asp Ser Gln Arg Thr Asp Glu Gly Asp

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155	153					85					90					95		
156	154																	
157 158 Gln Asn Pro Arg Arg Cys Lys Trp Thr Glu Pro Tyr Cys Val Ile Ala 159 115 120 125 160 161 Ala Val Lys Ile Phe Pro Arg Phe Phe Met Val Ala Lys Gln Cys Ser 162 130 135 140 163 164 Ala Gly Cys Ala Ala Met Glu Arg Pro Lys Pro Glu Glu Lys Arg Phe 165 145 150 150 155 160 166 167 Leu Leu Glu Glu Pro Met Pro Phe Phe Tyr Leu Lys Cys Cys Lys Ile 168 169 170 Arg Tyr Cys Asn Leu Glu Gly Pro Pro Ile Asn Ser Ser Val Phe Lys 171 180 185 190 172 173 Glu Tyr Ala Gly Ser Met Gly Glu Ser Cys Gly Gly Leu Trp Leu Ala 174 195 200 205 175 176 Ile Leu Leu Leu Leu Leu Ala Ser Ile Ala Ala Gly Leu Ser Leu Ser 177 210 215 220	155	-Asn	Arg	-Va-l-	Trp	-Cys	-His	Val	Cys	Glu	Arg	Glu	Asn	Thr	Phe	Glu	Cys	
158 Gln Asn Pro Arg Arg Cys Lys Trp Thr Glu Pro Tyr Cys Val Ile Ala 125	156				100					105					110			
159	157																	
160 161 Ala Val Lys Ile Phe Pro Arg Phe Phe Met Val Ala Lys Gln Cys Ser 162 130 135 140 163 164 Ala Gly Cys Ala Ala Met Glu Arg Pro Lys Pro Glu Glu Lys Arg Phe 165 145 150 155 160 166 167 Leu Leu Glu Glu Pro Met Pro Phe Phe Tyr Leu Lys Cys Cys Lys Ile 168 165 170 170 175 169 170 Arg Tyr Cys Asn Leu Glu Gly Pro Pro Ile Asn Ser Ser Val Phe Lys 171 180 185 190 172 173 Glu Tyr Ala Gly Ser Met Gly Glu Ser Cys Gly Gly Leu Trp Leu Ala 174 195 200 205 175 176 Ile Leu Leu Leu Leu Ala Ser Ile Ala Ala Gly Leu Ser Leu Ser 177 210 215 220	158	Gln	Asn	Pro	Arg	Arg	Cys	Lys	Trp	Thr	Glu	Pro	Tyr	Cys	Val	Ile	Ala	
161 Ala Val Lys Ile Phe Pro Arg Phe Phe Met Val Ala Lys Gln Cys Ser 162	159			115					120					125				
162	160																	
163 164 Ala Gly Cys Ala Ala Met Glu Arg Pro Lys Pro Glu Glu Lys Arg Phe 165 145 150 150 155 160 166 167 Leu Leu Glu Glu Pro Met Pro Phe Phe Tyr Leu Lys Cys Cys Lys Ile 168 165 170 170 175 169 170 Arg Tyr Cys Asn Leu Glu Gly Pro Pro Ile Asn Ser Ser Val Phe Lys 171 180 185 190 172 173 Glu Tyr Ala Gly Ser Met Gly Glu Ser Cys Gly Gly Leu Trp Leu Ala 174 195 200 205 175 176 Ile Leu Leu Leu Leu Ala Ser Ile Ala Ala Gly Leu Ser Leu Ser 177 210 220 188 179 180	161	Ala	Val	Lys	Ile	Phe	Pro	Arg	Phe	Phe	Met	Val	Ala	Lys	Gln	Cys	Ser	
164 Ala Gly Cys Ala Ala Met Glu Arg Pro Lys Pro Glu Glu Lys Arg Phe 165 145	162		130					135					140					
165	163																	
166 167 Leu Leu Glu Glu Pro Met Pro Phe Phe Tyr Leu Lys Cys Cys Lys Ile 168	164	Ala	Gly	Cys	Ala	Ala	Met	Glu	Arg	Pro	Lys	Pro	Glu	Glu	Lys	Arg		
167 Leu Leu Glu Glu Glu Pro Met Pro Met Pro Phe Phe Tyr Leu Lys Cys Cys Lys Ile 168 165 170 175 169 170 175 175 170 Arg Tyr Cys Asn Leu Glu Gly Pro Pro Ile Asn Ser Ser Val Phe Lys 185 190 171 180 185 190 190 172 173 Glu Tyr Ala Gly Ser Met Gly Glu Ser Cys Gly Gly Leu Trp Leu Ala 195 200 205 175 176 Ile Leu Leu Leu Leu Ala Ser Ile Ala Ala Gly Leu Ser Leu Ser 220 220 178 179 180 179 180 179 180	165	145					150					155					160	
168	166			-													_	
169 170 Arg Tyr Cys Asn Leu Glu Gly Pro Pro Ile Asn Ser Ser Val Phe Lys 171 180 185 190 172 173 Glu Tyr Ala Gly Ser Met Gly Glu Ser Cys Gly Gly Leu Trp Leu Ala 174 195 200 205 175 176 Ile Leu Leu Leu Ala Ser Ile Ala Ala Gly Leu Ser Leu Ser 177 210 215 220 178 179 180	167	Leu	Leu	Glu	Glu		Met	Pro	Phe	Phe	-	Leu	Lys	Cys	Cys	_	Ile	
170 Arg Tyr Cys Asn Leu Glu Gly Pro Pro Ile Asn Ser Ser Val Phe Lys 171 180 185 190 172 173 Glu Tyr Ala Gly Ser Met Gly Glu Ser Cys Gly Gly Leu Trp Leu Ala 174 195 200 205 175 176 Ile Leu Leu Leu Ala Ser Ile Ala Ala Gly Leu Ser Leu Ser 177 210 215 220 188 179 180	168					165					170					175		
171							_	_			_				_		_	
172 173 Glu Tyr Ala Gly Ser Met Gly Glu Ser Cys Gly Gly Leu Trp Leu Ala 174 195 200 205 175 176 Ile Leu Leu Leu Leu Ala Ser Ile Ala Ala Gly Leu Ser Leu Ser 177 210 215 220 178 179 180		Arg	Tyr	Cys		Leu	Glu	Gly	Pro		Ile	Asn	Ser	Ser		Phe	Lys	
173 Glu Tyr Ala Gly Ser Met Gly Glu Ser Cys Gly Gly Leu Trp Leu Ala 174 195 200 205 175 176 Ile Leu Leu Leu Ala Ser Ile Ala Ala Gly Leu Ser Leu Ser 177 210 215 220 178 179 180					180					185					190			
174 195 200 205 175 176 Ile Leu Leu Leu Ala Ser Ile Ala Ala Gly Leu Ser Leu Ser 177 210 215 220 178 179 180		_		_	_									_	_	_	- 5	
175 176 Ile Leu Leu Leu Ala Ser Ile Ala Ala Gly Leu Ser Leu Ser 177 210 215 220 178 179 180		Glu	Tyr		Gly	Ser	Met	Gly		Ser	Cys	Gly	Gly		Trp	Leu	Ala	
176 Ile Leu Leu Leu Ala Ser Ile Ala Ala Gly Leu Ser Leu Ser 177 210 215 220 178 179 180				195					200					205				
177 210 215 220 178 179 180				_	_	_		_					_	_	_	_		
178 179 180		Ile		Leu	Leu	Leu	Ala		ITe	ALA	Ala	GIY		ser	Leu	ser		
179 180			210					215					220					
180																		
181																		
	181																	

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/10/022,366

DATE: 01/17/2002 TIME: 06:57:45

INPUT SET: S36723.raw

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: Boehringer Mannheim GmbH
7	Unknown or Misplaced Identifier	(B) STREET: Sandhofer Str. 112-132
8	Unknown or Misplaced Identifier	(C) CITY: Mannheim
9	Unknown or Misplaced Identifier	(E) COUNTRY: Germany
10	Unknown or Misplaced Identifier	(F) POSTAL CODE: 68305
23	Wrong application Serial Number	(A) APPLICATION NUMBER:US/09/977,801

SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/10/022,366

DATE: 01/17/2002 TIME: 06:57:45

INPUT SET: S36723.raw

ADDRESSEE
STREET
CITY
STATE
COUNTRY
ZIP
CORRESPONDENCE ADDRESS
CLASSIFICATION